

FIGURE 1

cDNA sequence of wild type amFP486

ATGGCTCTTTCAAACAAGTTTATCGGAGATGACATGAAAATGACCTACCATATGGATG
GCTGTGTCAATGGGCATTACTTTACCGTCAAAGGTGAAGGCAACGGGAAGCCATACGA
AGGGACGCAGACCTCGACTTTTAAAGTCACCATGGCCAACGGTGGGCCCCTTGCATTC
TCCTTTGACATACTATCTACAGTGTTCAAGTATGGAAATCGATGCTTTACTGCGTATC
CTACCAGTATGCCCAGCTATTTCAAACAAGCATTTCTGACGGAATGTCATATGAAAG
GACTTTTACCTATGAAGATGGAGGAGTTGCTACAGCCAGTTGGGAAATAAGCCTTAAA
GGCAACTGCTTTGAGCACAAATCCACGTTTCATGGAGTGAACTTTCCTGCTGATGGAC
CTGTGATGGCGAAGATGACAACTGGTTGGGACCCATCTTTTGAGAAAATGACTGTCTG
CGATGGAATATTGAAGGGTGATGTCACCGCGTTCCTCATGCTGCAAGGAGGTGGCAAT
TACAGATGCCAATTCCACACTTCTTACAAGACAAAAAACCAGGTGACGATGCCACCAA
ACCATGCGGTGGAACATCGCATTGCGAGGACCGACCTTGACAAAGGTGGCAACAGTGT
TCAGCTGACGGAGCACGCTGTTGCACATATAACCTCTGTTGTCCCTTTC (SEQ ID
NO:01)

amino acid sequence of wild type amFP486

MALSNKFIGD DMKMTYHMDG CVNGHYFTVK GEGNGKPYEG TQTSTFKVTM ANGGPLAFSF
DILSTVFKYG NRCFTAYPTS MPDYFKQAFP DGMSYERTFT YEDGGVATAS WEISLKGNCF
EHKSTFHGVN FPDGPVMAK MTTGWDPSE KMTVCDGILK GDVTAFLMLQ GGGNYRCQFH
TSYKTKKPVT MPPNHAVEHR IARTDLKGG NSVQLTEHAV AHITSVVPF
(SEQ ID NO:02)

10006922-120401

Figure 2

cDNA sequence of wild type cFP484

TATAGGANCATNNGGGNGATTGGGGTCCAAAGCATTGTAACCAACGCAGATAACCCCCAG
 TGGTNTCAAACGCAGANAACCGGGGAACATTGGAAAATTGANTNTTAAGGAGGCAAGGAA
 TCGGGAGTAAAGTTGCGAGAACTGAAAAAATGAAGTGTAATTTGTGTTCTGCCTGTCC
 TTCTTGGTCCTCGCCATCACAAACGCGAACATTTTTTTGAGAAACGAGGCTGACTTAGAA
 GAGAAGACATTGAGAATACCAAAAGCTCTAACCACCATGGGTGTGATTAAACCAGACATG
 AAGATTAAGCTGAAGATGGAAGGAAATGTAAACGGGCATGCTTTTGTGATCGAAGGAGAA
 GGAGAAGGAAAGCCTTACGATGGGACACACACTTTAAACCTGGAAGTGAAGGAAGGTGCG
 CCTCTGCCTTTTTCTTACGATATCTTGTCAAACGCGTTCAGTACGGAACAGAGCATTG
 ACAAATACCCAGACGATATAGCAGACTATTTCAAGCAGTCGTTTCCCGAGGGATATTCC
 TGGGAAAGAACCATGACTTTTGAAGACAAAGGCATTGTCAAAGTGAAAAGTGACATAAGC
 ATGGAGGAAGACTCCTTTATCTATGAAATTCGTTTTGATGGGATGAACTTCTCTCCCAAT
 GGTCCGGTTATGCAGAAAAAACTTTGAAGTGGGAACCATCCACTGAGATTATGTACGTG
 CGTGATGGAGTGCTGGTCGGGAGATATTAGCCATTCTCTGTTGCTGGAGGGAGGTGGCCAT
 TACCGATGTGACTTCAAAAGTATTTACAAAGCAAAAAAGTTGTCAAATTGCCAGACTAT
 CACTTTGTGGACCATCGCATTGAGATCTTGAACCATGACAAGGATTACAACAAAGTAACG
 CTGTATGAGAATGCAGTTGCTCGCTATTCTTTGCTGCCAAGTCAGGCCCTAGACAACAAGG
 ATACTGAAAACATATTTGCTGAGGGTTTGTGTTGTTTTTAAAAGACATCAGCTCAGCA
 TTCGTTAGTTGTAACAAAAAATAGCTTTAATTTTTGGTGGGATTAAATCATAGGGATTG
 TTTTAGTAATCATTTTGCTTAATAAAAAGTGCCTTG (SEQ ID NO:03)

amino acid sequence of wild type cFP484

M K C K F V F C L S
 F L V L A I T N A N I F L R N E A D L E
 E K T L R I P K A L T T M G V I K P D M
 K I K L K M E G N V N G H A F V I E G E
 G E G K P Y D G T H T L N L E V K E G A
 P L P F S Y D I L S N A F Q Y G N R A L
 T K Y P D D I A D Y F K Q S F P E G Y S
 W E R T M T F E D K G I V K V K S D I S
 M E E D S F I Y E I R F D G M N F P P N
 G P V M Q K K T L K W E P S T E I M Y V
 R D G V L V G D I S H S L L L E G G G H
 Y R C D F K S I Y K A K K V V K L P D Y
 H F V D H R I E I L N H D K D Y N K V T
 L Y E N A V A R Y S L L P S Q A (SEQ ID NO:04)

F0402T 226900F

Figure 3

cDNA sequence of zFP506

ATGGCTCAGTCAAAGCACGGTCTAACAAAAGAAATGACAATGAAATACCGTATGGAAGGGTGC
GTCGATGGACATAAATTTGTGATCACGGGAGAGGGCATTGGATATCCGTTCAAAGGGAAACAG
GCTATTAATCTGTGTGTGGTTCGAAGGTGGACCATTTGCCATTTGCCGAAGACATATTGTCAGCT
GCCTTTATGTACGGAAACAGGGTTTTCACTGAATATCCTCAAGACATAGCTGACTATTTCAAG
AACTCGTGTCTGCTGGTTATACATGGGACAGGTCTTTTCTCTTTGAGGATGGAGCAGTTTGC
ATATGTAATGCAGATATAACAGTGAGTGTTGAAGAAAACATGCATGTATCATGAGTCCAAATTT
TATGGAGTGAATTTTCTGCTGATGGACCTGTGATGAAAAAGATGACAGATAACTGGGAGCCA
TCCTGCGAGAAGATCATAACAGTACCTAAGCAGGGGATATTGAAAGGGGATGTCTCCATGTAC
CTCCTTCTGAAGGATGGTGGGCGTTTACGGTGCCAATTCGACACAGTTTACAAAGCAAAGTCT
GTGCCAAGAAAGATGCCGGACTGGCACTTCATCCAGCATAAGCTCACCCGTGAAGACCGCAGC
GATGCTAAGAATCAGAAATGGCATCTGACAGAACATGCTATTGCATCCGGATCTGCATTGCCC
(SEQ ID NO:05)

amino acid sequence of zFP506

MAQSKHGLTK EMTMKYRM EG CVDGHK FVIT GEGIGY PFKG KQAINLCVVE GGPLPFAEDI LSAAFNYGNR VFTEYPQDIA
DYFKNSCPAG YTWDRSFLFE DGAVCICNAD ITVSVEENCM YHESKFYGVN FPADGPVMKK MTDNWEPSCE KIIPVPKQGI
LKGDVSMYLL LKDGGR LRCQ FDTVYKAKSV PRKMPDWHFI QHKL TREDRS DAKNQKWHLT EHAIASGSAL P
(SEQ ID NO:06)

F0402T 226900F

Figure 4

cDNA sequence of zFP538

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gagttgagtt tctcgacttc agttgtatca attttggggc atcaagcgat ctattttcaa
catggctcat tcaaagcacg gtctaaaaga agaaatgaca atgaaatacc acatggaagg
gtgcgtcaac ggacataaat ttgtgatcac gggcgaaggc attggatata cgttcaaagg
gaaacagact attaattctgt gtgtgatcga agggggacca ttgccatttt ccgaagacat
attgtcagct ggctttaagt acggagacag gattttcact gaatatacctc aagacatagt
agactatttc aagaactcgt gtcctgctgg atatacatgg ggcaggtcctt ttctctttga
ggatggagca gtctgcatat gcaatgtaga tataacagtg agtgtcaaag aaaactgcat
ttatcataag agcatattta atggaatgaa ttttcctgct gatggacctg tgatgaaaaa
gatgacaact aactgggaag catcctgcga gaagatcatg ccagtaccta agcaggggat
actgaaaggg gatgtctcca tgtacctcct tctgaaggat ggtgggctgtt accggtgcca
gttcgacaca gtttacaaag caaagtctgt gccaaagtaag atgccggagt ggcacttcac
ccagcataag ctctccgtg aagaccgcag cgatgctaag aatcagaagt ggcagctgac
agagcatgct attgcattcc cttctgcctt ggcttgataa gaatgtagtt ccaacatttt
aatgcatgtg cttgtcaatt attctgataa aaatgtagtt gagttgaaaa cagacaagta
caaataaagc acatgtaaat cgtct      (SEQ ID NO:07)

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amino acid sequence of zFP538

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Met Ala His Ser Lys His Gly Leu Lys Glu Glu Met Thr Met Lys
Tyr His Met Glu Gly Cys Val Asn Gly His Lys Phe Val Ile Thr
Gly Glu Gly Ile Gly Tyr Pro Phe Lys Gly Lys Gln Thr Ile Asn
Leu Cys Val Ile Glu Gly Gly Pro Leu Pro Phe Ser Glu Asp Ile
Leu Ser Ala Gly Phe Lys Tyr Gly Asp Arg Ile Phe Thr Glu Tyr
Pro Gln Asp Ile Val Asp Tyr Phe Lys Asn Ser Cys Pro Ala Gly
Tyr Thr Trp Gly Ser Phe Leu Phe Glu Asp Gly Ala Val Cys Ile
Cys Asn Val Asp Ile Thr Val Ser Val Lys Glu Asn Cys Ile Tyr
His Lys Ser Ile Phe Asn Gly Met Asn Phe Pro Ala Asp Gly Pro
Val Met Lys Lys Met Thr Thr Asn Trp Glu Ala Ser Cys Glu Lys
Ile Met Pro Val Pro Lys Gln Gly Ile Leu Lys Gly Asp Val Ser
Met Tyr Leu Leu Leu Lys Asp Gly Gly Arg Tyr Arg Cys Gln Phe
Asp Thr Val Tyr Lys Ala Lys Ser Val Pro Ser Lys Met Pro Glu
Trp His Phe Ile Gln His Lys Leu Leu Arg Glu Asp Arg Ser Asp
Ala Lys Asn Gln Lys Trp Gln Leu Thr Glu His Ala Ile Ala Phe
Pro Ser Ala Leu Ala (SEQ ID NO:08)

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10006922-120401

FIGURE 5

cDNA sequence of dsFP483

ACGGTCAGGGACACGGTGACCCACTTTGGTATTCTAACAAAATGAGTTGGTCCAAGAGTG
TGATCAAGGAAGAAATGTTGATCGATCTTCATCTGGAAGGAACGTTCAATGGGCACTACT
TTGAAATAAAAGGCAAAGGAAAAGGGAAGCCTAATGAAGGCACCAATACCGTCACGCTCG
AGGTTACCAAGGGTGGACCTCTGCCATTTGGTTGGCATATTTTGTGCCCACAATTTCACT
ATGGAAACAAGGCATTTGTCCACCACCCTGACGACATACCTGATTATCTAAAGCTGTCAT
TTCCGGAGGGATATACATGGGAACGGTCCATGCACCTTTGAAGACGGTGGCTTGTGTTGTA
TCACCAATGATATCAGTTTGACAGGCAACTGTTTCAACTACGACATCAAGTTCACCTGGCT
TGAACCTTCCTCCAAATGGACCCGTTGTGCAGAAGAAGACAACCTGGCTGGGAACCGAGCA
CTGAGCGTTTGTATCCTCGTGATGGCGTGTGATAGGAGACATCCATCATGCTCTCACAG
TGGAAGGAGGTGGTCATTACGTATGTGACATTAAACTGTTTACAGGGCCAAGAAGCCCG
TAAAGATGCCAGGGTATCACTATGTTGACACCAAACCTGGTTATAAGGAGCAACGACAAAG
AATTCATGAAAGTTGAGGAGCATGAAATCGCCGTTGCACGCCACCATCCGCTCCAAAGCC
AATGAAGCTTAAGTAAAGCAAAAAGGTGACGAGGCATGATAGTATGACATGATAGTATGA
CATGATAGTATGACATGATAGTAAGAATTGTAAGCAAAAAGGCTTTGCTTATTAAACTTGT
AATTGAAAAC (SEQ ID NO:09)

amino acid sequence of dsFP483

M S W S K S V
I K E E M L I D L H L E G T F N G H Y F
E I K G K G K G K P N E G T N T V T L E
V T K G G P L P F G W H I L C P Q F Q Y
G N K A F V H H P D D I P D Y L K L S F
P E G Y T W E R S M H F E D G G L C C I
T N D I S L T G N C F N Y D I K F T G L
N F P P N G P V V Q K K T T G W E P S T
E R L Y P R D G V L I G D I H H A L T V
E G G G H Y V C D I K T V Y R A K K P V
K M P G Y H Y V D T K L V I R S N D K E
F M K V E E H E I A V A R H H P L Q S Q
(SEQ ID NO:10)

10006922-120491

FIGURE 6

cdNA sequence of drFP583

ATGAGGTCTTCCAAGAATGTTATCAAGGAGTTTCATGAGGTTTAAAGGTTTCGCATGGAAGGAACGGTCAATGGGCACGAGT
 TTGAAATAGAAGGCGAAGGAGAGGGGAGGCCATACGAAGGCCACAATACCGTAAAGCTTAAGGTAACCAAGGGGGGACC
 TTTGCCATTTGCTTGGGATATTTTGTCAACCAATTTTCAGTATGGAAGCAAGGTATATGTCAAGCACCCCTGCCGACATA
 CCAGACTATAAAAAGCTGTCTATTTCTGAAGGATTTAAATGGGAAAGGGTCATGAACCTTTGAAGACGGTGGCGTTCGTTA
 CTGTAACCCAGGATTCAGTTTGCAGGATGGCTGTTTCATCTACAAGGTCAAGTTCATTGGCGTGAACCTTCCTTCCGA
 TGGACCTGTTTATGCAAAAGAAGACAATGGGCTGGGAAGCCAGCACTGAGCGTTTGTATCCTCGTGATGGCGTGTGAAA
 GGAGAGATTCTAAGGCTCTGAAGCTGAAAGACGGTGGTCATTACCTAGTTGAATTCAAAGTATTTACATGGCAAAGA
 AGCCTGTGCAGCTACCAGGGTACTACTATGTTGACTCCAACTGGATATAACAAGCCACAACGAAGACTATACAATCGT
 TGAGCAGTATGAAAGAACCGAGGGACGCCACCATCTGTTTCCTTTAA (SEQ ID NO:11)

cdNA sequence of drFP583.1

GTCCTCCCAAGCAGTGGTATCAACGCAGAGTACGGGGGAGTTTCAGCCAGTGACGGT
 CAGTGACAGGGTGAGCCACTTGGTATACCAACAAAATGAGGTCTTCCAAGAATGTTA
 TCAAGGAGTTTCATGAGGTTTAAAGGTTTCGCATGGAAGGAACGGTCAATGGGCACGAGT
 TTGAAATAGAAGGCGAAGGAGAGGGGAGGCCATACGAAGGCCACAATACCGTAAAGC
 TTAAGGTAACCAAGGGGGACCTTTGCCATTTGCTTGGGATATTTTGTCAACCAAT
 TTCAGTATGGAAGCAAGGTATATGTCAAGCACCCCTGCCGACATACCAGACTATAAAA
 AGCTGTCTATTTCTGAAGGATTTAAATGGGAAAGGGTCATGAACCTTTGAAGACGGTG
 GCGTCGTTACTGTAACCCAGGATTCCAGTTTGCAGGATGGCTGTTTCATCTACAAGT
 CAAGTTCATTGGCGTTGAACCTTTCCTTCCGATGGACCTGTTATGCAAAAGAAGACAA
 TGGGCTGGGAAGCCAGCACTGAGCGTTTGTATCCTCGTGATGGCGTGTGAAAGGAG
 AGATTCTAAGGCTCTGAAGCTGAAAGACGGTGGTCATTACCTAGTTGAATTCAAAA
 GTATTTACATGGCAAAGAAGCCTGTGCAGCTACCAGGGTACTACTATGTTGACTCCA
 AACTGGATATAACAAGCCACAACGAAGACTATACAATCGTTGAGCAGTATGAAAGAA
 CCGAGGGACGCCACCATCTGTTTCCTTTAAGGCTGAACCTTGGCTCAGACGTGGGTGAG
 CGGTAATGACCACAAAAGGCAGCGAAGAAAAACCATGATCGTTTTTTTTAGGTTGGC
 AGCCTGAAATCGTAGGAAATACATCAGAAATGTTACAAACAGG (SEQ ID NO:45)

amino acid sequence of drFP583

MRSSKNVIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAWDILSPQFQ
 YGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIYKVKFIGVNFPSD
 GPMVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSIYMAKKPVQLPGYYYYVDSK
 LDITSHNEDYTIVEQYERTEGRHHLFL SEQ ID NO:012)

amino acid sequence of drFP583.1

Met Arg Ser Ser Lys Asn Val Ile Lys Glu Phe Met Arg Phe Lys
 Val Arg Met Glu Gly Thr Val Asn Gly His Glu Phe Glu Ile Glu
 Gly Glu Gly Glu Gly Arg Pro Tyr Glu Gly His Asn Thr Val Lys
 Leu Lys Val Thr Lys Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile
 Leu Ser Pro Gln Phe Gln Tyr Gly Ser Lys Val Tyr Val Lys His
 Pro Ala Asp Ile Pro Asp Tyr Lys Lys Leu Ser Phe Pro Glu Gly
 Phe Lys Trp Glu Arg Val Met Asn Phe Glu Asp Gly Gly Val Val
 Thr Val Thr Gln Asp Ser Ser Leu Gln Asp Gly Cys Phe Ile Tyr
 Lys Ser Ser Ser Leu Ala Leu Asn Phe Pro Ser Asp Gly Pro Val
 Met Gln Lys Lys Thr Met Gly Trp Glu Ala Ser Thr Glu Arg Leu
 Gly His Tyr Leu Val Glu Phe Lys Ser Ile Ile Met Ala Lys Lys
 Pro Val Gln Leu Pro Gly Tyr Tyr Tyr Val Asp Ser Lys Leu Asp
 Ile Thr Ser His Asn Glu Asp Tyr Thr Ile Val Glu Gln Tyr Glu
 Arg Ser Glu Arg His His Leu Phe Leu
 (SEQ ID NO:46)

10006923 120401

FIGURE 7

Amino Acid and Nucleotide Sequence for asFP600

ATGGCTTCCTTTTTTAAAGAAGACTATGCCCTTTAAGACGACCATTGAAGGGACGGTTAATGGCCAC
TACTTCAAGTGTACAGGAAAAGGAGAGGGCAACCCATTTGAGGGTACGCAGGAAATGAAGATAGAG
GTCATCGAAGGAGGTCCATTGCCATTTGCCTTCCACATTTTGTCAACGAGTTGTATGTACGGTAGT
AAGGCCTTCATCAAGTATGTGTCAGGAATTCCTGACTACTTCAAGCAGTCTTCCCTGAAGGTTTT
ACTTGGGAAAAGAACCACAACCTACGAGGATGGAGGCTTTCTTACAGCTCATCAGGACACAAGCCTA
GATGGAGATTGCCTCGTTTTACAAGGTCAAGATTCTTGGTAATAATTTTCCTGCTGATGGCCCCGTG
ATGCAGAACAAAGCAGGAAGATGGGAGCCATCCACCGAGATAGTTTATGAAGTTGACGGTGTCTTG
CGTGGACAGTCTTTGATGGCCCTTAAGTGCCCTGGTGGTTCGTCATCTGACTTGCCATCTCCATACT
ACTTACAGGTCCAAAAAACCAGCTGCTGCCTTGAAGATGCCAGGATTTCAATTTTGAAGATCATCGC
ATCGAGATAATGGAGGAAGTTGAGAAAGGCAAGTGCTATAAACAGTACGAAGCAGCAGTGGGCAGG
TACTGTGATGCTGCTCCATCCAAGCTTGGACATAAC (SEQ ID NO:13)

Amino acid

MASFLKKTMP FKTITIEGTVN GHYFKCTGKG EGNPFEGTQE MKIEVIEGGP LPFAFHILST
SCMYGSKTFI KYVSGIPDYF KQSFPEGFTW ERTTTYEDGG FLTAHQDTSI DGDCLVYKVK
ILGNNFPADG PVMQNKAGRW EPATEIVYEV DGVLRGQSLM ALKCPGGRHL TCHLHTTYRS
KKPAAALKMP GFHFEDHRIE IMEEVEKGKC YKQYEAAGR YCDAAPSKLG HN (SEQ ID
NO:14)

10006922 120401

Figure 8

cdNA sequence of dgFP512

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attcacctcg gtgatttgta agagaaagga tcaccatcaa gagaagagct gtaaaagtta   60
atattttact gtactttctac cagcatgagt gcacttaaag aagaaatgaa aatcaacctt  120
acaatggaag gtgttggttaa cgggcttcca tttaagatcc gtgggggatgg aaaaggcaaa  180
ccataccagg gatcacagga gttaaccttg acggtggtta aaggcgggcc tctgcctttc  240
tcttatgata ttctgacaac gatgtttcag tacggcaaca gggcattcgt aaactaccca  300
gaggacatac cagatatttt caagcagacc tgttctggtc ctaatggtgg atattcctgg  360
caaaggacca tgacttatga agacggagggc gtttgcaactg ctacaagcaa catcagcgtg  420
gttgggcgaca ctttcaatta tgacattcac tttatgggag cgaattttcc tcttgatggg  480
ccagtgatgc agaaaagaac aatgaaatgg gaaccatcca ctgagataat gtttgaacgt  540
gatggaatgc tgaggggtga cattgccatg tctctgttgc tgaagggagg gggccattac  600
cgatgtgatt ttgaaactat ttataaaccc aataaggttg tcaagatgcc agattaccat  660
tttgtggacc actgcattga gataacgagt caacaggatt attacaacgt ggttgagctg  720
accgaggttg ctgaagcccg ctactcttcg ctggagaaaa tcggcaaadc aaaggcgtaa  780
atccaagcaa tctaagaaaa caacaaggca ttaaaccgaa tcaccgtttt gaatttttcg  840
ttcggaattt cttggtaaaa ctaggttttag aacgtttcat ttcgctggac ttctttgact  900
cagctgtaga caagaaaga                (SEQ ID NO:15)                919

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amino acid sequence of dgFP512

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Met Ser Ala Leu Lys Glu Glu Met Lys Ile Asn Leu Thr Met Glu
Gly Val Val Asn Gly Leu Pro Phe Lys Ile Arg Gly Asp Gly Lys
Gly Lys Pro Tyr Gln Gly Ser Gln Glu Leu Thr Leu Thr Val Val
Lys Gly Gly Pro Leu Pro Phe Ser Tyr Asp Ile Leu Thr Thr Met
Phe Gln Tyr Gly Asn Arg Ala Phe Val Asn Tyr Pro Glu Asp Ile
Pro Asp Ile Phe Lys Gln Thr Cys Ser Gly Pro Asn Gly Gly Tyr
Ser Trp Gln Arg Thr Met Thr Tyr Glu Asp Gly Gly Val Cys Thr
Ala Thr Ser Asn Ile Ser Val Val Gly Asp Thr Phe Asn Tyr Asp
Ile His Phe Met Gly Ala Asn Phe Pro Leu Asp Gly Pro Val Met
Gln Lys Arg Thr Met Lys Trp Glu Pro Ser Thr Glu Ile Met Phe
Glu Arg Asp Gly Met Leu Arg Gly Asp Ile Ala Met Ser Leu Leu
Leu Lys Gly Gly Gly His Tyr Arg Cys Asp Phe Glu Thr Ile Tyr
Lys Pro Asn Lys Val Val Lys Met Pro Asp Tyr His Phe Val Asp
His Cys Ile Glu Ile Thr Ser Gln Gln Asp Tyr Tyr Asn Val Val
Glu Leu Thr Glu Val Ala Glu Ala Arg Tyr Ser Ser Leu Glu Lys
Ile Gly Lys Ser Lys Ala
(SEQ ID NO:16)

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10006922 120401

cdna sequence of dmFP592

(SEQ ID NO:17)

[illegible]

(SEQ ID NO:18)

Figure 10

M A L S N E F I G D D M K M
 676 ATG GCC CTG TCC AAC GAG TTC ATC GGC GAC GAC ATG AAG ATG
 TAC CGG GAC AGG TTG TTC AAG TAG CCG CTG CTG TAC TTC TAC
 T Y H M D G C V N G H Y F T V
 721 ACC TAC CAC ATG GAC GGC TGC GTG AAC GGC CAC TAC TTC ACC GTG
 TGG ATG GTG TAC CTG CCG ACG CAC TTG CCG GTG ATG AAG TGG CAC
 K G E G S G K P Y E G T Q T S
 766 AAG GGC GAG GGC AGC GGC AAG CCC TAC GAG GGC ACC CAG ACC TCC
 TTC CCG CTC CCG TCG CCG TTC GGG ATG CTC CCG TGG GTC TGG AGG
 T F K V T M A N G G P L A F S
 811 ACC TTC AAG GTG ACC ATG GCC AAC GGC GGC CCC CTG GCC TTC TCC
 TGG AAG TTC CAC TGG TAC CGG TTG CCG CCG GGG GAC CGG AAG AGG
 F D I L S T V F M Y G N R C F
 856 TTC GAC ATC CTG TCC ACC GTG TTC ATG TAC GGC AAC CGC TGC TTC
 AAG CTG TAG GAC AGG TGG CAC AAG TAC ATG CCG TTG GCG ACG AAG
 T A Y P T S M P D Y F K Q A F
 901 ACC GCC TAC CCC ACC AGC ATG CCC GAC TAC TTC AAG CAG GCC TTC
 TGG CGG ATG GGG TGG TCG TAC GGG CTG ATG AAG TTC GTC CGG AAG
 P D G M S Y E R T F T Y E D G
 946 CCC GAC GGC ATG TCC TAC GAG AGA ACC TTC ACC TAC GAG GAC GGC
 GGG CTG CCG TAC AGG ATG CTC TCT TGG AAG TGG ATG CTC CTG CCG
 G V A T A S W E I S L K G N C
 991 GGC GTG GCC ACC GCC AGC TGG GAG ATC AGC CTG AAG GGC AAC TGC
 CCG CAC CGG TGG CGG TCG ACC CTC TAG TCG GAC TTC CCG TTG ACG
 F E H K S T F H G V N F P A D
 1036 TTC GAG CAC AAG TCC ACC TTC CAC GGC GTG AAC TTC CCC GCC GAC
 AAG CTC GTG TTC AGG TGG AAG GTG CCG CAC TTG AAG GGG CGG CTG
 G P V M A K K T T G W D P S F
 1081 GGC CCC GTG ATG GCC AAG AAG ACC ACC GGC TGG GAC CCC TCC TTC
 CCG GGG CAC TAC CGG TTC TTC TGG TGG CCG ACC CTG GGG AGG AAG
 E K M T V C D G I L K G D V T
 1126 GAG AAG ATG ACC GTG TGC GAC GGC ATC TTG AAG GGC GAC GTG ACC
 CTC TTC TAC TGG CAC ACG CTG CCG TAG AAC TTC CCG CTG CAC TGG
 A F L M L Q G G G N Y R C Q F
 1171 GCC TTC CTG ATG CTG CAG GGC GGC GGC AAC TAC AGA TGC CAG TTC
 CGG AAG GAC TAC GAC GTC CCG CCG CCG TTG ATG TCT ACG GTC AAG
 H T S Y K T K K P V T M P P N
 1216 CAC ACC TCC TAC AAG ACC AAG AAG CCC GTG ACC ATG CCC CCC AAC
 GTG TGG AGG ATG TTC TGG TTC TTC GGG CAC TGG TAC GGG GGG TTG
 H V V E H R I A R T D L D K G
 1261 CAC GTG GTG GAG CAC CGC ATC GCC AGA ACC GAC CTG GAC AAG GGC
 GTG CAC CAC CTC GTG GCG TAG CGG TCT TGG CTG GAC CTG TTC CCG
 G N S V Q L T E H A V A H I T
 1306 GGC AAC AGC GTG CAG CTG ACC GAG CAC GCC GTG GCC CAC ATC ACC
 CCG TTG TCG CAC GTC GAC TGG CTC GTG CGG CAC CGG GTG TAG TGG
 S V V P F *
 1351 TCC GTG GTG CCC TTC TGA
 AGG CAC CAC GGG AAG ACT

(SEQ ID NO:27 & 28)

10006922-120401

Figure 11

Non-aggregating mutant FP3-NA was generated from zFP506-N65M (non-humanized version). In comparison with zFP506-N65M, FP3-NA contains two additional amino acid substitutions - K5E and K10E. Also, one accidental nucleotide substitution was introduced due to PCR mistake (double underline).

Cloning into pQE30 was done using BamHI and HindIII sites:

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GGA TCC GCT CAG TCA GAG CAC GGT CTA ACA GAA GAA ATG ACA ATG AAA
BamHI  A  Q  S  E  H  G  L  T  E  E  M  T  M  K

TAC CGT ATG GAA GGG TGC GTC GAT GGA CAT AAA TTT GTG ATC ACG GGA
Y  R  M  E  G  C  V  D  G  H  K  F  V  I  T  G

GAG GGC ATT GGA TAT CCG TTC AAA GGG AAA CAG GCT ATT AAT CTG TGT
E  G  I  G  Y  P  F  K  G  K  Q  A  I  N  L  C

GTG GTC GAA GGT GGA CCA TTG CCA TTT GCC GAA GAC ATA TTG TCA GCT
V  V  E  G  G  P  L  P  F  A  E  D  I  L  S  A

GCC TTT ATG TAC GGA AAC AGG GTT TTC ACT GAA TAT CCT CAA GAC ATA
A  F  M  Y  G  N  R  V  F  T  E  Y  P  Q  D  I

GTT GAC TAT TTC AAG AAC TCG TGT CCT GCT GGA TAT ACA TGG GAC AGG
V  D  Y  F  K  N  S  C  P  A  G  Y  T  W  D  R

TCT TTT CTC TTT GAG GAT GGA GCA GTT TGC ATA TGT AAT GCA GAT ATA
S  F  L  F  E  D  G  A  V  C  I  C  N  A  D  I

ACA GTG AGT GTT GAA GAA AAC TGC ATG TAT CAT GAG TCC AAA TTC TAT
T  V  S  V  E  E  N  C  M  Y  H  E  S  K  F  Y

GGA GTG AAT TTT CCT GCT GAT GGA CCT GTG ATG AAA AAG ATG ACA GAT
G  V  N  F  P  A  D  G  P  V  M  K  K  M  T  D

AAC TGG GAG CCA TCC TGC GAG AAG ATC ATA CCA GTA CCT AAG CAG GGG
N  W  E  P  S  C  E  K  I  I  P  V  P  K  Q  G

ATA TTG AAA GGG GAT GTC TCC ATG TAC CTC CTT CTG AAG GAT GGT GGG
I  L  K  G  D  V  S  M  Y  L  L  L  K  D  G  G

CGT TTA CGG TGC CAA TTC GAC ACA GTT TAC AAA GCA AAG TCT GTG CCA
R  L  R  C  Q  F  D  T  V  Y  K  A  K  S  V  P

AGA AAG ATG CCG GAC TGG CAC TTC ATC CAG CAT AAG CTC ACC CGT GAA
R  K  M  P  D  W  H  F  I  Q  H  K  L  T  R  E

GAC CGC AGC GAT GCT AAG AAT CAG AAA TGG CAT CTG ACA GAA CAT GCT
D  R  S  D  A  K  N  Q  K  W  H  L  T  E  H  A

ATT GCA TCC GGA TCT GCA TTG CCC TGA AAGCTT
I  A  S  G  S  A  L  P  * HindIII (SEQ ID NO:29 & 30)

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T0006923-120401

Figure 12

Amino acid sequence of zFP506 Yellow mutant

MAQSKHGLTKEMTMKYRMEGCVDPGHKQVITGEGIGYPFKGKQAINLCVVEGGPLPFAEDILSAGFKYGDRVFTTEYPQDI
VDYFKNSCPAGYTWDRSFLFEDGAVCICNADITVSVEENCMYHESKFYGVNFPADGPVMKKMTDNWEPSCEKIIPVPKQ
GILKGDVSMYLLKDGGRRLRCQFDTVYKAKSVPRKMPDWHFIQHKLTREDRSDAKNQKWHLTEHAIASGSALP*
(SEQ ID NO:31)

Figure 13

Amino Acid Sequence of zFP506 Yellow/bright mutant

MAQSKHGLTKEMTMKYRMEGCVDPGHKQVITGEGIGYPFKGKQAINLCVVEGGPLPFAEDILSAGFKYGDRVFTTEYPQDI
VDYFKNSCPAGYTWDRSFLFEDGAVCICNADITVSVEENCMYHESKFYGVNFPADGPVMKKMTDNWEPSCEKIIPVPRQ
GILKGDVSMYLLKDGGRRLRCQFDTVYKAKSVPRKMPDWHFIQHKLTREDRSDAKNQKWHLTEHAIASGSALS*
(SEQ ID NO:32)

104027-2269007

Figure 14

Non-aggregating mutant FP4-NA was generated from zFP538-M128V (humanized version). In comparison with zFP538-M128V, FP4-NA contains two additional amino acid substitutions - K5E and K9T. Also, two accidental nucleotide substitutions were introduced due to PCR mistakes (double underline).

Cloning into pQE30 was done using BamHI and HindIII sites:

```

GGA TCC GCC CAC AGC GAG CAC GGC CTG ACC GAG GAG ATG ACC ATG AAG
BamHI  A  H  S  E  H  G  L  T  E  E  M  T  M  K

TAC CAC ATG GAG GGC TGC GTG AAC GGC CAC AAG TTC GTG ATC ACC GGC
Y  H  M  E  G  C  V  N  G  H  K  F  V  I  T  G

GAG GGC ATC GGC TAC CCC TTC AAG GGC AAG CAG ACC ATC AAC CTG TGC
E  G  I  G  Y  P  F  K  G  K  Q  T  I  N  L  C

GTG ATC GAG GGC GGC CCC CTG CCC TTC AGC GAG GAC ATC CTG AGC GCC
V  I  E  G  G  P  L  P  F  S  E  D  I  L  S  A

GGC TTC AAG TAC GGC GAC CGG ATC TTC ACC GAG TAC CCC CAG GAC ATC
G  F  K  Y  G  D  R  I  F  T  E  Y  P  Q  D  I

GTG GAC TAC TTC AAG AAC AGC TGC CCC GCC GGC TAC ACC TGG GGC CGG
V  D  Y  F  K  N  S  C  P  A  G  Y  T  W  G  R

AGC TTC CTG TTC GAG GAC GGC GCC GTG TGC ATC TGT AAC GTG GAC ATC
S  F  L  F  E  D  G  A  V  C  I  C  N  V  D  I

ACC GTG AGC GTG AAG GAG AAC TGC ATC TAC CAC AAG AGC ATC TTC AAC
T  V  S  V  K  E  N  C  I  Y  H  K  S  I  F  N

GGC GTG AAC TTC CCC GCC GAC GGC CCC GTG ATG AAG AAG ATG ACC ACC
G  V  N  F  P  A  D  G  P  V  M  K  K  M  T  T

AAC TGG GAG GCC AGC TGC GAG AAG ATC ATG CCC GTG CCT AAG CAG GGC
N  W  E  A  S  C  E  K  I  M  P  V  P  K  Q  G

ATC CTG AAG GGC GAC GTG AGC ATG TAC CTG CTG CTG AAG GAC GGC GGC
I  L  K  G  D  V  S  M  Y  L  L  L  K  D  G  G

CGG TAC CGG TGC CAG TTC GAC ACC GTG TAC AAG GCC AAG AGC GTG CCC
R  Y  R  C  Q  F  D  T  V  Y  K  A  K  S  V  P

AGC AAG ATG CCC GAG TGG CAC TTC ATC CAG CAC AAG CTG CTG CGG GAG
S  K  M  P  E  W  H  F  I  Q  H  K  L  L  R  E

GAC CGG AGC GAC GCC AAG AAC CAG AAG TGG CAG CTG ACC GAG CAC GCC
D  R  S  D  A  K  N  Q  K  W  Q  L  T  E  H  A

ATC GCC TTC CCC AGC GCC CTG GCC TGA AAGCTT
I  A  F  P  S  A  L  A  * HindIII (SEQ ID NOS: 33-34)

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10006922-120401

Figure 15

All mutants are derived from drFP583 (called "pink" or FP6.) by random mutagenesis

The mutants E57 and AG4 are derivative from E5

Mutant: E5 = V105A, S197T Phenotype: in *E.coli* seen as Green overnight, matures

to Red over 24h at 37°C (final peaks ratio Red vs. Green is 75:25); folding is faster than FP6.

Mutant: E8 = N42H Phenotype: always has two peaks Green & Red in approx. 60:40; folding is faster than E5 (about 8h at 37°C)

Mutant: E83 = N42H, V71A, I180V Phenotype: always has two almost equal peaks Green & Red; folding is the same as for E8

Mutant: E5up = V105A Phenotype: seen as Red from the beginning; folding is faster than E5 (about 12-16h) Almost no Green peak at final point of maturation

Mutant: E57 = V105A, I161T, S197A Phenotype: at common is like E5up but folding is more faster (no more that 8-10h) Very small Green peak at final point of maturation (less that 5%)

Mutant: E5down = S197T Phenotype and folding rate are exactly the same as for E5

Mutant: AG4 = V71M, V105A, S197T Phenotype: Very bright Green, no Red at all (even at the beginning); folding is faster than E5 (no more that 16h)

Mutant: AG4 = V71M, V105A, Y120H, S197T Phenotype: at common is like AG4, but more brighter (approx. twice) one.

| | | |
|-----|---|-----|
| 1 | Met Arg Ser Ser Lys Asn Val Ile Lys Glu Phe Met Arg Phe Lys Val | 16 |
| 1 | ATG CGC TCC TCC AAG AAC GTC ATC AAG GAG TTC ATG CGC TTC AAG GTG | 48 |
| 17 | Arg Met Glu Gly Thr Val Asn Gly His Glu Phe Glu Ile Glu Gly Glu | 32 |
| 49 | CGC ATG GAG GGC ACC GTG AAC GGC CAC GAG TTC CAG ATC GAG GGC GAG | 96 |
| | His(CAC) for E8 and E83 | |
| 33 | Gly Glu Gly Arg Pro Tyr Glu Gly His Asn Thr Val Lys Leu Lys Val | 48 |
| 97 | GGC GAG GGC CGC CCC TAC GAG GGC CAC AAC ACC GTG AAG CTG AAG GTG | 144 |
| 49 | Thr Lys Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln | 64 |
| 145 | ACC AAG GGC GGC CCC CTG CCC TTC GCC TGG GAC ATC CTG TCC CCC CAG | 192 |
| | Met(ATG) for AG4 and AG45/Ala(GCG) for E83 | |
| 65 | Phe Gln Tyr Gly Ser Lys Val Tyr Val Lys His Pro Ala Asp Ile Pro | 80 |
| 193 | TTC CAG TAC GGC TCC AAG GTG TAC GTG AAG CAC CCC GCC GAC ATC CCC | 240 |
| 81 | Asp Tyr Lys Lys Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Val | 96 |
| 241 | GAC TAC AAG AAG CTG TCC TTC CCC GAG GGC TTC AAG TGG GAG CGC GTG | 288 |
| | Ala(GCG) -for E5, E57, AG4 and AG45 | |
| 97 | Met Asn Phe Glu Asp Gly Gly Val Val Thr Val Thr Gln Asp Ser Ser | 112 |
| 289 | ATG AAC TTC GAG GAC GGC GGC GTG GTG ACC GTG ACC CAG GAC TCC TCC | 336 |
| | His(CAC) -for AG45 | |
| 113 | Leu Gln Asp Gly Cys Phe Ile Tyr Lys Val Lys Phe Ile Gly Val Asn | 128 |
| 337 | CTG CAG GAC GGC TGC TTC ATC TAC AAG GTG AAG TTC ATC GGC GTG AAC | 384 |
| 129 | Phe Pro Ser Asp Gly Pro Val Met Gln Lys Lys Thr Met Gly Trp Glu | 144 |
| 385 | TTC CCC TCC GAC GGC CCC GTG ATG CAG AAG AAG ACC ATG GGC TGG GAG | 432 |
| 145 | Ala Ser Thr Glu Arg Leu Tyr Pro Arg Asp Gly Val Leu Lys Gly Glu | 160 |
| 433 | GCC TCC ACC GAG CGC CTG TAC CCC CGC GAC GGC GTG CTG AAG GGC GAG | 480 |
| | Thr(ACC) for E57 | |
| 161 | Ile His Lys Ala Leu Lys Leu Lys Asp Gly Gly His Tyr Leu Val Glu | 176 |
| 481 | ATC CAC AAG GCC CTG AAG CTG AAG GAC GGC GGC CAC TAC CTG GTG GAG | 528 |
| | Val(GTC) for E83 | |
| 177 | Phe Lys Ser Ile Tyr Met Ala Lys Lys Pro Val Gln Leu Pro Gly Tyr | 192 |
| 529 | TTC AAG TCC ATC TAC ATG GCC AAG AAG CCC GTG CAG CTG CCC GGC TAC | 576 |
| | Thr(ACC) for E5, AG4 and AG45/Ala(GCC) for E57 | |
| 193 | Tyr Tyr Val Asp Ser Lys Leu Asp Ile Thr Ser His Asn Glu Asp Tyr | 208 |
| 577 | TAC TAC GTG GAC TCC AAG CTG GAC ATC ACC TCC CAC AAC GAG GAC TAC | 624 |
| 209 | Thr Ile Val Glu Gln Tyr Glu Arg Thr Glu Gly Arg His His Leu Phe Leu *** | 229 |
| 625 | ACC ATC GTG GAG CAG TAC GAG CGC ACC GAG GGC CGC CAC CAC CTG TTC CTG TAA | 678 |

(SEQ ID NO:11 & 12)

1006922.120401

FIGURE 16

Nucleic acid sequence of humanized drFP583

ATGGTGCCTCCTCCAAGAACGTCATCAAGGAGTTCATGCGCTTCAAGGTGCGCATGG
AGGGCACCGTGAACGGCCACGAGTTCGAGATCGAGGGCGAGGGCGAGGGCCGCCCC
TACGAGGGCCACAACACCGTGAAGCTGAAGGTGACCAAGGGCGGCCCCCTGCCCTTC
GCCTGGGACATCCTGTCCCCCAGTTCAGTACGGCTCCAAGGTGTACGTGAAGCACC
CCGCCGACATCCCCGACTACAAGAAGCTGTCTTCCCCGAGGGGCTTCAAGTGGGAGC
GCGTGATGAACCTTCGAGGACGGCGGCGTGGTGACCGTGACCCAAGACTCCTCCCTGC
AGGACGGCTGCTTCATCTACAAGGTGAAGTTCATCGGCGTGAACCTCCCTCCGACGG
CCCCGTAATGCAGAAGAAGACCATGGGCTGGGAGGCCTCCACCGAGCGCCTGTACCC
CCGCGACGGCGTGCTGAAGGGCGAGATCCACAAGGCCCTGAAGCTGAAGGACGGCG
GCCACTACCTGGTGGAGTTCAAGTCCATCTACATGGCCAAGAAGCCCGTGACGCTGCC
CGGCTACTACTACGTGGACTCCAAGCTGGACATCACCTCCCACAACGAGGACTACAC
CATCGTGGAGCAGTACGAGCGCACCGAGGGCCGCCACCACCTGTTCTGTAG (SEQ ID
NO:35)

Figure 17

DNA sequence (ORF) of E5-NA

ATGGCCTCCTCCGAGAACGTCATCACCGAGTTCATGCGCTTCAAGGTGCGCATGGAGGGCACCGTGAACGGCCACGAGT
TCGAGATCGAGGGCGAGGGCGAGGGCCGCCCCCTACGAGGGCCACAACACCGTGAAGTTGAAGGTGACCAAGGGCGGCCC
CCTGCCCTTCGCCTGGGACATCCTGTCCCCCAGTTCAGTACGGCTCCAAGGTGTACGTGAAGCACCCTCCGACATC
CCCGACTACAAGAAGCTGTCTTCCCCGAGGGGCTTCAAGTGGGAGCGCGTGATGAACCTTCGAGGACGGCGGCGTGGCGA
CCGTGACCCAGGACTCCTCCCTGCAGGACGGCTGCTTCATCTACAAGGTGAAGTTCATCGGCGTGAACCTCCCTCCGA
CGCCCCGTGATGCAGAAGAAGACCATGGGCTGGGAGGCCTCCACCGAGCGCCTGTACCCCGCGACGGCGTGCTGAAG
GGCGAGATCCACAAGGCCCTGAAGCTGAAGGACGGCGGCCACTACCTGGTGGAGTTCAAGTCCATCTACATGGCCAAGA
AGCCCGTGACGCTGCCCGGCTACTACTACGTGGACACCAAGCTGGACATCACCTCCCACAACGAGGACTACACCATCGT
GGAGCAGTACGAGCGCACCGAGGGCCGCCACCACCTGTTCTGTAA (SEQ ID NO:36)

Figure 18

ATGGTGCCTCCTCCAAGAA CGTCATCAAG GAGTTCATGC GCTTCAAGGT
GCGCATGGAGGGCACCGTGA ACGGCCACGA GTTCGAGATC GAGGGCGAGG GCGAGGGCCG
CCCCTACGAG GGCCACAACA CCGTGAAGCT GAAGGTGACC AAGGGCGGCC CCCTGCCCTT
CGCCTGGGAC ATCCTGTCCC CCCAGTTCCA GTACGGCTCC AAGGTGTACG TGAAGCACC
CGCCGACATC CCCGACTACA AGAAGCTGTC CTTCCCCGAG GGCTTCAAGT GGGAGCGCGT
GATGAACCTTCGAGGACGGCG GCGTGGCGAC CGTGACCAA GACTCCTCCC TGCAGGACGG
CTGCTTCATC TACAAGGTGA AGTTCATCGG CGTGAACCTC CCCTCCGACG GCCCCGTAAT
GCAGAAGAAG ACCATGGGCT GGGAGGCCTC CACCGAGCGC CTGTACCCCC GCGACGGCGT
GCTGAAGGGC GAGACCCACA AGGCCCTGAA GCTGAAGGAC GGCGGCCACT ACCTGGTGGA
GTTCAAGTCC ATCTACATGG CCAAGAAGCC CGTGCAGCTG CCCGGCTACT ACTACGTGGA
CGCCAAGCTG GACATCACCT CCCACAACGA GGAATACACC ATCGTGGAGC AGTACGAGCG
CACCGAGGGCCGCCACCACC TGTTCTGTAA G (SEQ ID NO:37)

10006922-120404

Figure 19.

Nucleic acid sequence FP6 (E57)-NA

ATGGCCTCCTCCGAGAACGTCATCACCGAGTTCATGCGCTTCAAGGTGCGCATGGAGGGCACCGTGA
ACGGCCACGAGTTCGAGATCGAGGGCGAGGGCGAGGGCCGCCCTACGAGGGCCACAACACCGTG
AAGCTGAAGGTGACCAAGGGCGGCCCTGCCCTTCGCCTGGGACATCCTGTCCCCCAGTTCAGT
ACGGCTCCAAGGTGTACGTGAAGCACCCCGCCGACATCCCCGACTACAAGAAGCTGTCCTTCCCCGA
GGGCTTCAAGTGGGAGCGCGTGATGAACTTCGAGGACGGCGGCGTGCGGACCGTGACCCAGGACTC
CTCCCTGCAGGACGGCTGCTTCATCTACAAGGTGAAGTTCATCGGCGTGAAGTTCCTCCCTCCGACGGC
CCCGTGATGCAGAAGAAGACCATGGGCTGGGAGGCCTCCACCGAGCGCCTGTACCCCCGCGACGGC
GTGCTGAAGGGCGAGACCCACAAGGCCCTGAAGCTGAAGGACGGCGGCCACTACCTGGTGGAGTTC
AAGTCCATCTACATGGCCAAGAAGCCCGTGACGCTGCCCGGCTACTACTACGTGGACGCCAAGCTGG
ACATCACCTCCACAACGAGGACTACACCATCGTGGAGCAGTACGAGCGCACCGAGGGCCGCCACCA
CCTGTTCTG (SEQ ID NO:38)

T04027 "22690001

Non-aggregating mutant FP7-NA was generated from M35-5 (FP7a). In comparison with M35-5, FP7-NA contains two additional substitutions - K6T and K7E. Nucleotide substitutions in the codon for Leu-4 were introduced to optimize codon usage (double underline).

[illegible]

FIGURE 21

ATG GCC TCC **TTC** CTG AAG AAG **ACC** ATG CCC TTC **AAG** ACC ACC ATC GAG
 M A S F L K K T M P F K T T I E

 GGC ACC GTG AAC GGC CAC TAC TTC AAG TGC ACC GGC AAG GGC GAG GGC
 G T V N G H Y F K C T G K G E G

 AAC CCC **TTC** GAG GGC ACC CAG GAG ATG **AAG** ATC GAG GTG ATC GAG GGC
 N P F E G T Q E M K I E V I E G

 GGC CCC CTG CCC TTC GCC TTC CAC ATC CTG TCC ACC TCC TGC ATG TAC
 G P L P F A F H I L S T S C M Y

 GGC TCC AAG GCC TTC ATC AAG TAC **GTG** TCC GGC ATC CCC GAC TAC TTC
 G S K A F I K Y V S G I P D Y F

 AAG CAG TCC **TTC** CCC GAG GGC TTC ACC TGG GAG CGC ACC ACC ACC TAC
 K Q S F P E G F T W E R T T T Y

 GAG GAC GGC GGC **TTC** CTG ACC GCC CAC CAG GAC ACC TCC CTG GAC GGC
 E D G G F L T A H Q D T S L D G

 GAC TGC CTG GTG TAC AAG GTG AAG ATC CTG GGC AAC AAC TTC CCC GCC
 D C L V Y K V K I L G N N F P A

 GAC GGC CCC GTG ATG CAG AAC AAG GCC GGC CGC TGG GAG CCC TCC ACC
 D G P V M Q N K A G R W E P S T

 GAG ATC GTG TAC GAG GTG GAC GGC GTG CTG CGC GGC CAG TCC CTG ATG
 E I V Y E V D G V L R G Q S L M

 GCC CTG **AAG** TGC CCC GGC GGC CGC CAC CTG ACC TGC CAC CTG CAC ACC
 A L K C P G G R H L T C H L H T

 ACC TAC CGC TCC AAG AAG CCC GCC TCC GCC CTG AAG ATG CCC GGC TTC
 T Y R S K K P A S A L K M P G F

 CAC TTC GAG GAC CAC CGC ATC GAG **ATC** **ATG** GAG GAG GTG GAG AAG GGC
 H F E D H R I E I M E E V E K G

 AAG TGC TAC AAG CAG TAC GAG GCC GCC GTG GGC CGC TAC TGC **GAC** GCC
 K C Y K Q Y E A A V G R Y C D A

 GCC CCC TCC AAG CTG GGC CAC AAC TgA
 A P S K L G H N * (SEQ ID NO:41 & 42)

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Figure 22

Sequence of humanized 6/9 hybrid gene and 6/9-Q3 mutant

| for 6/9-2G and 6/9-Q3 CAG(Q) | | | | | | | | | | | | | | | | | |
|------------------------------|-----|-----|------------|-----|-----|-----|-----|-----|------------|-----|-----|-----|-----|-----|------------|-----|-----|
| 1 | ATG | AGC | TGC | AGC | AAG | AAC | GTG | ATC | AAG | GAG | TTC | ATG | CGG | TTC | AAG | GTG | 48 |
| 1 | M | S | C | S | K | N | V | I | K | E | F | M | R | F | <u>K</u> | V | 16 |
| 49 | CGG | ATG | GAG | GGC | ACC | GTG | AAC | GGC | CAC | GAG | TTC | GAG | ATC | AAG | GGC | GAG | 96 |
| 17 | R | M | E | G | T | V | N | G | H | E | F | E | I | K | G | E | 32 |
| 97 | GGC | GAG | GGC | CGG | CCC | TAC | GAG | GGC | CAC | TGC | AGC | GTG | AAG | CTC | ATG | GTG | 144 |
| 33 | G | E | G | R | P | Y | E | G | H | C | S | V | K | L | M | V | 48 |
| 145 | ACC | AAG | GGC | GGC | CCC | CTC | CCC | TTC | GCC | TTC | GAC | ATC | CTC | AGC | CCC | CAG | 192 |
| 49 | T | K | G | G | P | L | P | F | A | F | D | I | L | S | P | Q | 64 |
| 193 | TTC | CAG | TAC | GGC | AGC | AAG | GTG | TAC | GTG | AAG | CAC | CCC | GCC | GAC | ATC | CCC | 240 |
| 65 | F | Q | Y | G | S | K | V | Y | V | K | H | P | A | D | I | P | 80 |
| ATG(M) for 6/9-Q3 | | | | | | | | | | | | | | | | | |
| 241 | GAC | TAC | AAG | AAG | CTC | AGC | TTC | CCC | GAG | GGC | TTC | AAG | TGG | GAG | CGG | GTG | 288 |
| 81 | D | Y | <u>K</u> | K | L | S | F | P | E | G | F | K | W | E | R | V | 96 |
| 289 | ATG | AAC | TTC | GAG | GAC | GGC | GGC | GTG | GTG | ACC | GTG | AGC | CAG | GAC | AGC | AGC | 336 |
| 97 | M | N | F | E | D | G | G | V | V | T | V | S | Q | D | S | S | 112 |
| 337 | CTC | AAG | GAC | GGC | TGC | TTC | ATC | TAC | GAG | GTG | AAG | TTC | ATC | GGC | GTG | AAC | 384 |
| 113 | L | K | D | G | C | F | I | Y | E | V | K | F | I | G | V | N | 128 |
| 385 | TTC | CCC | AGC | GAC | GGC | CCC | GTG | ATG | CAG | CGG | CGG | ACC | CGG | GGC | TGG | GAG | 432 |
| 129 | F | P | S | D | G | P | V | M | Q | R | R | T | R | G | W | E | 144 |
| 433 | GCC | AGC | AGC | GAG | CGG | CTC | TAC | CCC | CGG | GAC | GGC | GTG | CTC | AAG | GGC | GAC | 480 |
| 145 | A | S | S | E | R | L | Y | P | R | D | G | V | L | K | G | D | 160 |
| 481 | ATC | CAC | ATG | GCC | CTC | CGG | CTC | GAG | GGC | GGC | GGC | CAC | TAC | CTC | GTG | GAG | 528 |
| 161 | I | H | M | A | L | R | L | E | G | G | G | H | Y | L | V | E | 176 |
| 529 | TTC | AAG | AGC | ATC | TAC | ATG | GCC | AAG | AAG | CCC | GTG | CAG | CTC | CCC | GGC | TAC | 576 |
| 177 | F | K | S | I | Y | M | A | K | K | P | V | Q | L | P | G | Y | 192 |
| 577 | TAC | TAC | GTG | GAC | AGC | AAG | CTC | GAC | ATC | ACC | AGC | CAC | AAC | GAG | GAC | TAC | 624 |
| 193 | Y | Y | V | D | S | K | L | D | I | T | S | H | N | E | D | Y | 208 |
| TCC(S) for 6/9-2G and 6/9-Q3 | | | | | | | | | | | | | | | | | |
| 625 | ACC | ATC | GTG | GAG | CAG | TAC | GAG | CGG | ACC | GAG | GGC | CGG | CAC | CAC | CTC | TTC | 672 |
| 209 | T | I | V | E | Q | Y | E | R | <u>T</u> | E | G | R | H | H | L | F | 224 |
| 673 | CTC | TGA | | | | | | | | | | | | | | | 678 |
| 225 | L | * | | | | | | | | | | | | | | | 226 |

(SEQ ID NO:43 & 44)

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